

<!--StartFragment-->RESULT 2

ABA00656

ID ABA00656 standard; cDNA; 3400 BP.

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AC ABA00656;

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DT 19-FEB-2003 (first entry)

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DE Human ENZM-4 cDNA, incyte ID No: 3535146CB1.

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KW Gene; ENZM; cardiovascular disorder; arteriovenous fistula; prostate;
KW atherosclerosis; hypertension; Raynaud's disease; aneurysm; cervix;
KW varicose vein; thrombophlebitis; congestive heart failure; brain; breast;
KW angina pectoris; ischaemic; heart disease; autoimmune; inflammation;
KW acquired immunodeficiency syndrome; anaemia; asthma; Crohn's disease;
KW neurological disorder; epilepsy; Huntington's disease; dementia; stroke;
KW Alzheimer's disease; Creutzfeldt-Jakob disease; multiple sclerosis;
KW cerebral palsy; Parkinson's disease; anxiety; schizophrenia; amnesia;
KW metabolic disorder; Addison's disease; goitre; infection; sarcoma;
KW pneumonia; hepatitis; influenza; immune deficiency; thymic dysplasia;
KW severe combined immunodeficiency disease; reproduction; infertility;
KW endometriosis; prostatitis; Peyronie's disease; impotence; eye disorder;
KW glaucoma; ocular hypertension; cell proliferation; psoriasis; myeloma;
KW polycythemia vera; cancer; adenocarcinoma; leukemia; lymphoma; melanoma;
KW MDMCSF; ss.

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OS Homo sapiens.

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FH Key Location/Qualifiers

FT CDS 66. .3002

FT /*tag= a

FT /product= "ENZM-4 protein"

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PN WO200283873-A2.

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PD 24-OCT-2002.

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PF 10-APR-2002; 2002WO-US015253.

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PR 13-APR-2001; 2001US-0283793P.

PR 16-MAY-2001; 2001US-0291544P.

PR 25-MAY-2001; 2001US-0293572P.

PR 27-JUL-2001; 2001US-0308182P.

PR 09-AUG-2001; 2001US-0311447P.

PR 29-AUG-2001; 2001US-0315874P.

PR 14-SEP-2001; 2001US-0322181P.

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PA (INCY-) INCYTE GENOMICS INC.

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Qy 1 ATGGGCACGCGTCTGCCGCTCGTCCTGCGCCAGCTCCGCCGCCCGCCCCAGCCCCCGGGC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 66 ATGGGCACGCGTCTGCCGCTCGTCCTGCGCCAGCTCCGCCGCCCGCCCCAGCCCCCGGGC 125

Qy	61	CCTCCGCGCCGCCTCCGTGTGCCCTGTTCGCGCTAGCAGCGGCGGCGGCGGAGGCGGCGGC	120
Db	126	CCTCCGCGCCGCCTCCGTGTGCCCTGTTCGCGCTAGCAGCGGCGGCGGCGGAGGCGGCGGC	185
Qy	121	GGTGGCCGGGAGGGCCTGCTTGGACAGCGGCGGCCGCAGGATGGCCAGGCCCGGAGCAGC	180
Db	186	GGTGGCCGGGAGGGCCTGCTTGGACAGCGGCGGCCGCAGGATGGCCAGGCCCGGAGCAGC	245
Qy	181	TGCAGCCCCGGCGGCCGAACGCCCGCGGCGGGACTCCATCGTCAGAGAAGTCATTTCAG	240
Db	246	TGCAGCCCCGGCGGCCGAACGCCCGCGGCGGGACTCCATCGTCAGAGAAGTCATTTCAG	305
Qy	241	AATTCAAAAGAAGTTCTAAGTTTATTGCAAGAAAAAAACCCTGCCTTCAAGCCGGTTCTT	300
Db	306	AATTCAAAAGAAGTTCTAAGTTTATTGCAAGAAAAAAACCCTGCCTTCAAGCCGGTTCTT	365
Qy	301	GCAATTATCCAGGCAGGTGACGACAACCTTGATGCAGGAAATCAACCAGAATTTGGCTGAG	360
Db	366	GCAATTATCCAGGCAGGTGACGACAACCTTGATGCAGGAAATCAACCAGAATTTGGCTGAG	425
Qy	361	GAGGCTGGTCTGAACATCACTCACATTTGCCTCCCTCCAGATAGCAGTGAAGCCGAGATT	420
Db	426	GAGGCTGGTCTGAACATCACTCACATTTGCCTCCCTCCAGATAGCAGTGAAGCCGAGATT	485
Qy	421	ATAGATGAAATCTTAAAGATCAATGAAGATACCAGAGTACATGGCCTTGCCCTTCAGATC	480
Db	486	ATAGATGAAATCTTAAAGATCAATGAAGATACCAGAGTACATGGCCTTGCCCTTCAGATC	545
Qy	481	TCTGAGAACTTGTTTAGCAACAAAGTCCTCAATGCCTTGAAACCAGAAAAAGATGTGGAT	540
Db	546	TCTGAGAACTTGTTTAGCAACAAAGTCCTCAATGCCTTGAAACCAGAAAAAGATGTGGAT	605
Qy	541	GGAGTAACAGACATAAACCTGGGGAAGCTGGTGCAGGGGATGCCCATGAATGTTTTGTT	600
Db	606	GGAGTAACAGACATAAACCTGGGGAAGCTGGTGCAGGGGATGCCCATGAATGTTTTGTT	665
Qy	601	TCACCTGTTGCCAAAGCTGTAATTGAACTTCTTGAAAAATCAGGTGTCAACCTAGATGGA	660
Db	666	TCACCTGTTGCCAAAGCTGTAATTGAACTTCTTGAAAAATCAGGTGTCAACCTAGATGGA	725
Qy	661	AAGAAGATTTTGGTAGTGGGGGCCCATGGGTCTTTGGAAGCTGCTCTACAATGCCTGTTC	720
Db	726	AAGAAGATTTTGGTAGTGGGGGCCCATGGGTCTTTGGAAGCTGCTCTACAATGCCTGTTC	785
Qy	721	CAGAGAAAAGGGTCCATGACAATGAGCATCCAGTGGAACACGCCAGCTTCAAAGCAAG	780
Db	786	CAGAGAAAAGGGTCCATGACAATGAGCATCCAGTGGAACACGCCAGCTTCAAAGCAAG	845

Qy	781	CTTCACGAGGCTGACATTGTGGTCCTAGGCTCACCTAAGCCAGAAGAGATTCCCCTTACT	840
Db	846	CTTCACGAGGCTGACATTGTGGTCCTAGGCTCACCTAAGCCAGAAGAGATTCCCCTTACT	905
Qy	841	TGGATACAACCAGGAACTACTGTTCTCAACTGCTCCCATGACTTCCTGTCAGGGAAGGTT	900
Db	906	TGGATACAACCAGGAACTACTGTTCTCAACTGCTCCCATGACTTCCTGTCAGGGAAGGTT	965
Qy	901	GGGTGTGGCTCTCCAAGAATACATTTTGGTGGACTCATTGAGGAAGATGATGTGATTCTC	960
Db	966	GGGTGTGGCTCTCCAAGAATACATTTTGGTGGACTCATTGAGGAAGATGATGTGATTCTC	1025
Qy	961	CTTGCTGCAGCTCTGCGAATTCAGAACATGGTCAGTAGTGGAAGGAGATGGCTTCGTGAA	1020
Db	1026	CTTGCTGCAGCTCTGCGAATTCAGAACATGGTCAGTAGTGGAAGGAGATGGCTTCGTGAA	1085
Qy	1021	CAGCAGCACAGGCGGTGGAGACTTCACTGCTTGAAACTTCAGCCTCTCTCCCCTGTGCCA	1080
Db	1086	CAGCAGCACAGGCGGTGGAGACTTCACTGCTTGAAACTTCAGCCTCTCTCCCCTGTGCCA	1145
Qy	1081	AGTGACATTGAGATTTCAAGAGGACAAACTCCAAAAGCTGTGGATGTCCTTGCCAAGGAG	1140
Db	1146	AGTGACATTGAGATTTCAAGAGGACAAACTCCAAAAGCTGTGGATGTCCTTGCCAAGGAG	1205
Qy	1141	ATTGGATTGCTTGCAGATGAAATTGAAATCTATGGCAAAAGCAAAGCCAAAGTACGTTTG	1200
Db	1206	ATTGGATTGCTTGCAGATGAAATTGAAATCTATGGCAAAAGCAAAGCCAAAGTACGTTTG	1265
Qy	1201	TCCGTGCTAGAAAGGTAAAGGATCAAGCAGATGGAAAATACGTCTTAGTTGCTGGGATC	1260
Db	1266	TCCGTGCTAGAAAGGTAAAGGATCAAGCAGATGGAAAATACGTCTTAGTTGCTGGGATC	1325
Qy	1261	ACACCCACCCCTCTTGGAGAAGGGAAGAGCACAGTCACCATCGGGCTTGTGCAGGCTCTG	1320
Db	1326	ACACCCACCCCTCTTGGAGAAGGGAAGAGCACAGTCACCATCGGGCTTGTGCAGGCTCTG	1385
Qy	1321	ACCGCACACCTGAATGTCAACTCCTTTGCCTGCTTGAGGCAGCCTTCCCAAGGACCGACG	1380
Db	1386	ACCGCACACCTGAATGTCAACTCCTTTGCCTGCTTGAGGCAGCCTTCCCAAGGACCGACG	1445
Qy	1381	TTTGGAGTGAAAGGAGGAGCCGCGGGTGGTGGATATGCCCAGGTCATCCCCATGGAGGAG	1440
Db	1446	TTTGGAGTGAAAGGAGGAGCCGCGGGTGGTGGATATGCCCAGGTCATCCCCATGGAGGAG	1505
Qy	1441	TTCAACCTTCACTTGACTGGAGACATCCACGCCATCACCGCTGCCAATAACTTGCTGGCT	1500
Db	1506	TTCAACCTTCACTTGACTGGAGACATCCACGCCATCACCGCTGCCAATAACTTGCTGGCT	1565
Qy	1501	GCCGCCATCGACACGAGGATTCTTCATGAAAACACGCAAACAGATAAGGCTCTGTATAAT	1560

Db	1566	 GCCGCCATCGACACGAGGATTCTTCATGAAAACACGCAAACAGATAAGGCTCTGTATAAT	1625
Qy	1561	CGGCTGGTTCCTTTAGTGAATGGTGTCTAGAGAATTTTCAGAAATTCAGCTTGCTCGGCTA	1620
Db	1626	 CGGCTGGTTCCTTTAGTGAATGGTGTCTAGAGAATTTTCAGAAATTCAGCTTGCTCGGCTA	1685
Qy	1621	AAAAAACTGGGAATAAATAAGACTGATCCGAGCACACTGACAGAAGAGGAAGTGAGTAAA	1680
Db	1686	 AAAAAACTGGGAATAAATAAGACTGATCCGAGCACACTGACAGAAGAGGAAGTGAGTAAA	1745
Qy	1681	TTTGCCCGTCTCGACATCGACCCATCTACCATCACGTGGCAGAGAGTATTGGATACAAAT	1740
Db	1746	 TTTGCCCGTCTCGACATCGACCCATCTACCATCACGTGGCAGAGAGTATTGGATACAAAT	1805
Qy	1741	GACCGATTTCTACGAAAAATAACCATCGGGCAGGGAAACACAGAGAAGGGCCATTACCGG	1800
Db	1806	 GACCGATTTCTACGAAAAATAACCATCGGGCAGGGAAACACAGAGAAGGGCCATTACCGG	1865
Qy	1801	CAGGCGCAGTTTGACATCGCAGTGGCCAGCGAGATCATGGCGGTGCTGGCCCTGACGGAC	1860
Db	1866	 CAGGCGCAGTTTGACATCGCAGTGGCCAGCGAGATCATGGCGGTGCTGGCCCTGACGGAC	1925
Qy	1861	AGCCTCGCAGACATGAAGGCACGGCTGGGAAGGATGGTGGTGGCCAGTGACAAAAGCGGG	1920
Db	1926	 AGCCTCGCAGACATGAAGGCACGGCTGGGAAGGATGGTGGTGGCCAGTGACAAAAGCGGG	1985
Qy	1921	CAGCCTGTGACAGCAGATGATTTGGGGGTGACAGGTGCTTTGACAGTTTTGATGAAAGAT	1980
Db	1986	 CAGCCTGTGACAGCAGATGATTTGGGGGTGACAGGTGCTTTGACAGTTTTGATGAAAGAT	2045
Qy	1981	GCAATAAAACCAAACCTGATGCAGACCCTGGAAGGGACACCTGTGTTTCGTGCATGCGGGC	2040
Db	2046	 GCAATAAAACCAAACCTGATGCAGACCCTGGAAGGGACACCTGTGTTTCGTGCATGCGGGC	2105
Qy	2041	CCTTTTGCTAACATTGCTCACGGCAACTCTTCAGTGTTGGCTGATAAAATTGCCCTGAAA	2100
Db	2106	 CCTTTTGCTAACATTGCTCACGGCAACTCTTCAGTGTTGGCTGATAAAATTGCCCTGAAA	2165
Qy	2101	CTGGTTGGTGAAGAAGGATTTGTAGTGACCGAAGCTGGCTTTGGTGCTGACATCGGAATG	2160
Db	2166	 CTGGTTGGTGAAGAAGGATTTGTAGTGACCGAAGCTGGCTTTGGTGCTGACATCGGAATG	2225
Qy	2161	GAGAAATTCTTCAACATCAAGTGCCGAGCTTCCGGCTTGGTGCCCAACGTGGTTGTGTTA	2220
Db	2226	 GAGAAATTCTTCAACATCAAGTGCCGAGCTTCCGGCTTGGTGCCCAACGTGGTTGTGTTA	2285
Qy	2221	GTGGCAACGGTGCAGCTCTGAAGATGCATGGAGGCGGGCCAAGTGTAACGGCTGGTGTT	2280

Db	2286	GTGGCAACGGTGCAGCTCTGAAGATGCATGGAGGCGGGCCAAGTGTAACGGCTGGTGTT	2345
Qy	2281	CCTCTTAAGAAAGAATATACAGAGGAGAACATCCAGCTGGTGGCAGACGGCTGCTGTAAC	2340
Db	2346	CCTCTTAAGAAAGAATATACAGAGGAGAACATCCAGCTGGTGGCAGACGGCTGCTGTAAC	2405
Qy	2341	CTCCAGAAGCAAATTCAGATCACTCAGCTCTTTGGGGTTCCCGTTGTGGTGGCTCTGAAT	2400
Db	2406	CTCCAGAAGCAAATTCAGATCACTCAGCTCTTTGGGGTTCCCGTTGTGGTGGCTCTGAAT	2465
Qy	2401	GTCTTCAAGACCGACACCCGCGCTGAGATTGACTTGGTGTGTGAGCTTGCAAAGCGGGCT	2460
Db	2466	GTCTTCAAGACCGACACCCGCGCTGAGATTGACTTGGTGTGTGAGCTTGCAAAGCGGGCT	2525
Qy	2461	GGTGCCTTTGATGCAGTCCCCTGCTATCACTGGTCGGTTGGTGAAAAGGATCGGTGGAC	2520
Db	2526	GGTGCCTTTGATGCAGTCCCCTGCTATCACTGGTCGGTTGGTGAAAAGGATCGGTGGAC	2585
Qy	2521	TTGGCTCGGGCTGTGAGAGAGGCTGCGAGTAAAAGAAGCCGATTCCAGTTCCTGTATGAT	2580
Db	2586	TTGGCTCGGGCTGTGAGAGAGGCTGCGAGTAAAAGAAGCCGATTCCAGTTCCTGTATGAT	2645
Qy	2581	G TTCAGGT TCCAATTGTGGACAAGATAAGGACCATTGCTCAGGCTGTCTATGGAGCCAAA	2640
Db	2646	G TTCAGGT TCCAATTGTGGACAAGATAAGGACCATTGCTCAGGCTGTCTATGGAGCCAAA	2705
Qy	2641	GATATTGAACTCTCTCCTGAGGCACAAGCCAAAATAGATCGTTACACTCAACAGGGTTTT	2700
Db	2706	GATATTGAACTCTCTCCTGAGGCACAAGCCAAAATAGATCGTTACACTCAACAGGGTTTT	2765
Qy	2701	GGAAATTTGCCCATCTGCATGGCAAAGACCCACCTTTCTCTATCTCACCAACCTGACAAA	2760
Db	2766	GGAAATTTGCCCATCTGCATGGCAAAGACCCACCTTTCTCTATCTCACCAACCTGACAAA	2825
Qy	2761	AAAGGTGTGCCAAGGGACTTCATCTTACCTATCAGTGACGTCCGGGCCAGCATAGGCGCT	2820
Db	2826	AAAGGTGTGCCAAGGGACTTCATCTTACCTATCAGTGACGTCCGGGCCAGCATAGGCGCT	2885
Qy	2821	GGGTTCATTTACCCTTTGGTCGGAACGATGAGCACCATGCCAGGACTGCCACCCGGCCC	2880
Db	2886	GGGTTCATTTACCCTTTGGTCGGAACGATGAGCACCATGCCAGGACTGCCACCCGGCCC	2945
Qy	2881	TGCTTTTATGACATAGATCTTGATAACCGAAACAGAACAAGTTAAAGGCTTGTTT	2934
Db	2946	TGCTTTTATGACATAGATCTTGATAACCGAAACAGAACAAGTTAAAGGCTTGTTT	2999

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